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Patentanmeldung Nr. Patent application No. Demande de brevet n°

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Der Präsident des Europäischen Patentamts:  
Im Auftrag

For the President of the European Patent Office

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**Blatt 2 der Bescheinigung  
Sheet 2 of the certificate  
Page 2 de l'attestation**

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A p-53 binding protein called Mdmx and encoding sequences for said protein

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Title: A novel p-53 binding protein called Mdmx and encoding sequences for said protein.

The present invention relates to molecular biology techniques and especially to their application in cancer research. In particular a method to identify new proteins associating to the p53 tumor suppressor protein, with some  
5 examples of cDNAs isolated this way is disclosed. It also relates to the results of said method, which are novel proteins having affinity for p53, as well as genes and other nucleic acid molecules encoding these novel proteins.

In particular the invention also relates to one such a  
10 novel protein and its encoding sequences, which protein has homology with the Mdm2 protein and which therefor has been designated as Mdmx.

The process by which a normal cell is transformed into a tumorigenic cell that can grow out to form a tumor is a very  
15 complex process in which several independent genetic changes have to take place. These genetic alterations can be roughly divided into two classes. The first comprises the genetic changes that alter the abundancy or properties of a gene product in such a way that it constitutively stimulates cell  
20 growth. The second class comprises genetic alterations that inhibit the normal cell growth controlling function of a gene product. An important role in the switch from normal cell to tumor cell is assigned to a protein called p53.

The protein called p53 has properties of both classes.  
25 Mutations in the p53 gene as found in human tumors abolish the tumor suppressor activity of the protein. In addition, several mutated forms of the p53 protein can have a dominant stimulating effect on cell growth.

Alterations in the p53 coding sequence are observed in  
30 over 50% of all human tumors. This makes p53 mutations the most frequent observed alteration in human cancer.

Many functional studies on p53 indicate that alterations in the p53-controlled functions can be very important for the

genesis and progression of a tumor. Mouse model studies show that either overexpression of a mutant p53 gene or inactivation of the normal wild-type p53 gene results in the development of tumors somewhere between the age of 3 and 6 months.

In humans it has been found that an hereditary form of cancer, the Li-Fraumeni Syndrome, is associated with a germ-line mutation in one allele of the p53 gene. In the tumors the remaining wild-type allele has been lost, indicating the importance of loss of wild-type p53 function for carcinogenesis.

One of the ways in which P53 probably functions is by guarding the integrity of the genome of cells. It can do so in two ways, namely through influencing the cell cycle and/or the process of repairing DNA damage and secondly by influencing the apoptosis pathway.

In the event that cells have received a dose of a DNA damaging agent, like ionizing radiation or some chemicals like cisplatin, p53 can arrest the cell in the cell cycle. The p53 protein may also be involved in the repair of the DNA. The presence of DNA damage results in an increase of the p53 protein levels through protein stabilization. Subsequently, the increased levels of p53 result in the activation of transcription of a set of p53-responsive genes. Two of the most important p53-responsive genes identified so far are the gene coding for an inhibitor of the cyclin-dependent kinases cdc2, cdk2, cdk4 and cdk6, and a gene called gadd45. The cdk-inhibitor is called p21<sup>Cip1</sup>/waf1, and is a member of an expanding family of cdk-inhibitors. These inhibitors inactivate the cdk's by direct binding. The activity of the cdk's, in conjunction with their appropriate cyclin partner, is essential for the progression through the cell cycle. Thus, by increasing the p21<sup>Cip1</sup>/waf1 expression, p53 blocks the cell cycle progression and arrests the cells in the G1 phase mainly. The current hypothesis is that this cell cycle delay allows the cell to repair its DNA before the DNA synthesis starts up and introduces mutations at the sites of the DNA

damage. The second p53-responsive gene important in this respect is the gadd45 gene. It has been shown that (over)expression of gadd45 also blocks cell cycle progression and it has been suggested that gadd45 might have a direct role in stimulating the process of DNA repair.

The second process p53 is involved in that is important for maintaining genomic integrity is apoptosis or programmed cell death. Apoptosis is a very ordered, active process that eventually results in the death of a cell. The process is very important in embryogenesis to get rid of superfluous cells. Recently more and more evidence has accumulated showing that interference with the apoptotic pathways can be very important for a cell to become a tumor cell. In addition, a successful treatment of tumors might depend on the possibility to induce an apoptotic pathway in the tumor cells. Two *in vivo* studies underscoring the notion that p53 is involved in apoptosis have been most informative. First, it was found that transgenic mice expressing an SV40 largeT mutant which can only bind and inactivate members of the retinoblastoma family (p105<sup>RB</sup>, p107, p130) but which has no effect on p53 function, develop tumors of the choroid plexus epithelium, but only very slowly compared to mice expressing the wild-type T-antigen. However, the same transgene can induce the development of rapidly growing tumors in p53-deficient mice. Comparison of the slowly growing and rapidly growing tumors revealed that the slowly growing tumors contained a significant percentage of apoptotic cells, which could hardly be found in the rapidly growing tumors. In another mouse model it was found that treatment of tumors lacking any functional p53 with X-rays or adriamycin hardly affected the tumor growth, while tumors containing a wild-type p53 but otherwise comparable could be eradicated. Analysis of both types of tumors after treatment showed the induction of apoptosis in the wild-type p53 containing tumor cells but not in the cells lacking p53. The mechanism by which p53 induces apoptosis has not been completely solved yet. On the one hand, high levels of p53 can lead to induction of expression of a gene called Bax-1 that has been shown to

stimulate apoptosis. On the other hand, a correlation between the induction of p53-dependent apoptosis and transcription repression by p53 has been found. It could be that both activation and repression of transcription by p53 is necessary  
5 to get efficient induction of apoptosis. In addition, cell type specificity in the mechanism by which p53 activates apoptosis is well possible.

The above thus gives an indication on the importance of p53 in suppressing tumor activity and possible mechanisms for  
10 said suppression. It also gives an indication of the effects of the absence of functional p53 for instance through mutations in the coding region of p53.

Apart from mutations in the coding region of p53, inhibition of the tumor suppressor function of the wild-type  
15 p53 can also occur through an altered-cytoplasmic- subcellular localization. The underlying mechanism for this retainment of the protein in the cytoplasm is unknown.

A third way to abolish the p53 tumor suppressor function is through complexation with another cellular protein called  
20 Mdm2. The gene encoding this protein was originally isolated from a mouse double-minute present in a spontaneously transformed Balb 3T3 cell line and shown to be responsible for the transformation. Later, it was found that a protein binding to p53 was exactly the same Mdm2 protein. In the transformed  
25 cells Mdm2 probably acts by binding to the p53 protein and inactivating its tumor suppressor function. In addition, it has been shown that binding of Mdm2 to p53 completely inhibits the capacity of p53 to activate transcription of a reported gene containing a p53-consensus DNA binding site in its  
30 promoter region. Interestingly, the transcription of the mdm2 gene is also stimulated by increased p53 levels. In that way a kind of feedback loop is established between Mdm2 and p53. Functions for Mdm2 apart from the inhibition of p53 activity are not clear. On the one hand an activity as transcription  
35 factor has been suggested, both because of its primary protein sequence that shows some Zinc-fingers possibly involved in DNA binding and because the Mdm2 protein has been found to

associate to the TATA-Binding Protein (TBP). This is the first protein to bind to TATA-containing promoters in the assembly of the basic transcription machinery complex. In addition, it has been reported that Mdm2 can effect the function of another transcription factor important in processes related to cancer, E2F-1. The activity of E2F-1 as a transcription factor is normally controlled by another tumor suppressor protein, the product encoded by the retinoblastoma predisposing gene. Active E2F-1 can activate the transcription of genes encoding proteins that stimulate cell growth, like the myc oncogene. Mdm2-overexpression, mainly through amplification of the gene, has been observed in a significant percentage of certain tumor types, establishing a role for this gene in carcinogenesis.

In conclusion, it is clear that a complete elucidation of the p53-controlled pathways and the identification of genes/proteins involved in these pathways can be very beneficial for understanding the onset and/or development of cancer. One way to understand more of p53 functions is to find out whether p53 has other cellular partners apart from Mdm2 that affect its tumor suppressor activity. An at this moment very widely used method to identify new proteins associating to a protein of interest is the yeast two-hybrid method. With the use of this method in literature two genes have been described coding for p53-associating proteins. However, the molecular functions of these proteins and their putative involvement in carcinogenesis are unknown as yet. Other methods to identify systematically new p53-associating proteins have not been described in literature.

Thus, it is clear that the development of another way to provide us with genes coding for proteins binding to p53 can be very important for understanding the p53 functions and the process of carcinogenesis. The present invention provides a method to arrive at proteins binding to p53 and the elucidation of their encoding genes.

One aspect of the present invention is the application of a method partly known in itself for the isolation of

associating proteins for the identification of (new) p53-  
associating gene products.

A first step in the methods according to the invention is  
the high level expression of the p53 protein in bacteria, with  
5 subsequent purification and radioactive labelling of the p53  
protein.

A second step is the use of the labeled p53 protein as a  
probe to screen cDNA expression libraries to pick up  
associating proteins and subsequently the isolation of the  
10 encoding cDNAs.

In a further aspect of the invention the resulting  
nucleic acids (such as cDNA's) encoding the novel associating  
proteins and the proteins themselves are provided.  
In figures 2a and 2b partial sequences of novel nucleic acids  
15 encoding such novel proteins are given. Figure 3 gives a novel  
cDNA sequence encoding another such novel protein which we  
have called Mdmx.

This last one is called Mdmx because of its homology to  
Mdm2.

20 The longest cDNA isolated sofar is 1701 nucleotides, and  
contains an open reading frame of 489 amino acids, exactly the  
same as the mouse mdm2 open reading frame.

The cDNA given in figure 3 is of mouse origin. It will be  
clear that using the present invention other mammalian species  
25 will be shown to have a counterpart of the Mdmx gene. These  
counterparts are of course included in the present invention.  
Especially because of the recently developed techniques such  
as PCR, it will be within the skilled man's ability to  
identify these counterparts and to design functional  
30 equivalents and/or fragments of the novel gene and its  
products.

It can be seen in fig. 4 that especially the N-terminal  
part of the Mdmx protein is very similar with the Mdm2  
protein. It has been shown that the N-terminal 100 amino acids  
35 in the Mdm/\*2 protein are essential for the binding to the p53  
protein. This result indicates a certain conservation in p53  
binding domains in different proteins, suggesting that other



proteins might contain such a domain as well. Furthermore, a strong conservation of two metal-binding domains in the C-terminal halve of the protein is found. This conservation suggests an important function for this part of the protein, possibly in binding to DNA/RNA or to other proteins.

The third conserved motif is a possible nucleotide binding site (GKT) at amino acid positions 451-453. (Fig 4; amino acid sequence of the putative Mmdx protein, and a comparison with the mouse and the human Mdm2 protein)

All the applications which have and can be envisaged for Mdm2 proteins or their encoding nucleic acids or parts thereof can of course be applied for Mdmx as well.

For instance, it can be envisioned that the Mdmx gene product(s), like the Mdm2 protein, has a role in certain types of cancer. Therefore, the status of the mdmx gene and the expression level can be monitored. This can be performed in several ways. First, the putative overexpression can be a result of gene amplification. This can be investigated by Southern blotting. We have already performed a pilot study to examine possible amplification of the mdmx gene in primary neuroblastomas and in neuroblastoma cell lines. Equal amounts of paired DNAs of normal and tumor tissue from a patient were digested with restriction enzymes, fractionated on a agarose gel, blotted onto nylon membranes and probed with a <sup>32</sup>P-labeled fragment of the human mdmx cDNA.

Results so far do not show any indication for amplification of the mdmx gene in neuroblastoma. To be certain a larger panel of tumors and cell lines has to be analyzed.

Another way to investigate overexpression of the gene is by quantitative RT-PCR analysis of the mRNA expression level in the tumors. The primers mentioned earlier that amplify a specific band of human mRNA could be used for this purpose.

The last method to analyze mdmx expression is at the protein level. Antibodies raised against the protein can be used, if necessary after purification, for in situ histochemistry studies on frozen sections or paraffin-embedded tissues. These types of experiments will give both an answer

as to the level and the localization of the protein in the cell.

Since it is not unlikely that Mdmx (over)expression plays a role in the development in (some types of) cancer, it may be important to be able to block Mdmx function in a cell. If the function is to bind and inactivate p53, this interaction could theoretically be relieved by introducing into the cell an overdose of peptide from the Mdmx domain that is necessary for the association to p53. Through competition the binding will be blocked.

Another possibility is to develop mutants of mdmx that can act dominant-negative on the wild-type protein. Possible target domains for mutations are the putative nucleotide binding site and the putative metal-binding motifs. These mutants can be cloned in viral expression vectors (retrovirus, adenovirus, AAV) for delivery to the target cells. It is still possible that MDMX does not inactivate p53, but actually enhances the functions of p53 or is an intermediate in the p53 functional pathways. If that turns out to be the case, not a mutant but a wild-type mdmx gene will be cloned in the expression vectors mentioned above and be delivered to the target cells.

From the comparison between Mdm2 and Mdmx proteins it can be concluded that some of the amino acids in the p53-binding domain are more important than others. We want to use this knowledge to develop primer sets that might amplify other genes containing a p53-binding domain from the same family.

### Experimental

#### 30 Cloning of the human wild-type p53 sequence into bacterial expression vector

The coding region for the wild-type human p53 protein was amplified by PCR with primers containing a KpnI site at the 5' end and a SacI site at the 3'-end. After amplification and cutting the fragment with the mentioned restriction enzymes the resulting DNA fragment was cloned into a SacI and KpnI-digested modified version of the pET-15b vector obtained from

Novagen. This modified vector contains 5' of the cloning sites a DNA sequence coding for five aminoacids (RRASV) that is recognized as a phosphorylation site for the Heart Muscle Kinase. Downstream from the cloning sites a sequence coding for 6 histidines is present.

As a result a fusion p53 protein can be synthesized in bacteria, containing at its N-terminal end a peptide stretch with a phosphorylation site for the Heart Muscle Kinase (Sigma) and at its C-terminal end a stretch of six histidines that allows purification over a nickel chelate column (Pharmacia). Figure 1 shows the main features of the p53 expression vector.

#### Production, purification and radioactive labelling of bacterially produced p53 protein

After construction the plasmid was propagated in the bacterial strain HB101, and subsequently transformed into the E. coli B-strain BL21(DE3) or this strain containing pLYSE. The induction of protein expression has essentially been performed according to the pET system manual provided by Novagen. In short, a BL21(DE3) colony containing the p53 expression plasmid was grown at 37°C to OD<sub>600</sub> of 0.6. IPTG was added to a final concentration of 1mM and incubation was continued for another 3 h. After cooling on ice the cells were harvested by centrifugation at 4°C at 5000 x g for 10 min. Cells were grown for additional four hours and pelleted by centrifugation for 10 min at 5000xg. The pellet was rinsed with ice cold PBS and resuspended in IMAC- 5 (20 mM Tris pH 8, 0.5 M NaCl, 5 mM Imidazole, 10 µg/ml PMSF (phenylmethylsulfonyl fluoride). The bacteria were lysed on ice by sonication (3x30 s.) and centrifuged at 20.000xg for 30 min at 4°C. It turned out that over 90% of the produced p53 protein was retained in the pellet. Bacterial pellet of insoluble proteins including p53 was incubated in IMAC-5 with 6 M urea for 30 minutes on ice. After centrifugation for 30 minutes at 30.000xg the urea was removed from the soluble fraction with the use of a 10DG desalting column (Bio-Rad).

The p53 fusion protein was purified using nickel chelate chromatography according to manufacture instructions (Novagen).

5 The column was washed with increasing concentrations of imidazole (10,20,40, 100 and 200 nM). Coomassie staining of a SDS-PAGE gel indicated that the protein eluted at 200 nM imidazole was over 70% pure.

10 For screening an expression library purified protein was radioactively labeled with the HMK( Sigma) and  $^{32}\text{P}$ -ATP according to the manufacturers protocol. Unincorporated radioactive nucleotides were removed with the use of a Sephadex G-25 column equilibrated with PBS/1% non-fatty dry milk. The protein could be labeled to a specific activity of  $> 10^7$  cpm per microgram protein.

15

Screening of expression library with radioactive labeled p53 protein

A cDNA library from a 16-day-old mouse embryo was obtained from Novagen. The cDNAs had been cloned into the  
20 lambda EX10x vector from Novagen and transformed into the E.coli strain BL21(DE3)pLysE. Approximately  $10^6$  phages were plated onto 15 150 mm dishes. Dishes were incubated at  $37^\circ\text{C}$  for 3-4 hours. When the plaques has become visible, 0.45  $\mu\text{m}$  nitrocellulose filters (Schleicher and Schüll) soaked in 10 mM  
25 IPTG were placed over the plaques and proteins were allowed to transfer overnight. Filter hybridization has been performed essentially as described by Ayer et al. (Cell 72, 211-222, 1993). Shortly, the filters were blocked for several hours in HBB/5% NFDM [20 mM HEPES (pH 7.5), 50 mM KCl, 10 mM  $\text{MgCl}_2$ , 10  
30 mM  $\beta$ -glycerol phosphate, 1 mM DTT, 0.1% NP-40 and 5% non-fatty dry milk]. Hybridization was performed overnight with at least  $2 \times 10^5$  cpm/ml p53 probe in [20 mM HEPES(pH 7.5), 50 mM KCl, 10 mM  $\text{MgCl}_2$ , 10 mM  $\beta$ -glycerol phosphate, 10 mM DTT, 0.1% NP-40 and 10% glycerol] at  $4^\circ\text{C}$ . After hybridization the  
35 filters were washed once in PBS containing 0.2% Triton X-100 for 10 minutes, and three additional washes were done in PBS, 0.2% Triton X-100, 100 mM KCl, for 15-20 minutes at  $4^\circ\text{C}$ .

After washing the filters were allowed to air dry, wrapped in Saran wrap and exposed to X-ray films.

Results: isolation of three cDNAs

5

The initial screen yielded 10 possible positive clones. After a second and third round screen, only three positive lambda clones remained. A purified phage preparation was introduced into the E.coli strain BM25.8 (Novagen). Through  
10 the Cre-loxP autosubcloning system, plasmids containing the insert are generated. PCR analysis of the three positive clones with the use of primers from the flanking vector sequences showed inserts of approximately 600, 800 and 1700 bp (named clone 1, 2 and 3, respectively). The first two clones  
15 were partially sequenced; the DNA sequence obtained showed no significant homology to any known sequence submitted to the several databases. (Fig 2; partial sequence of two smaller clones, clone 1 and clone 2).

The sequence of the third clone showed clear homology  
20 with a cloned human gene called mdm2. This is to date the only human gene whose gene product can bind to and inactivate the tumor suppressor function of p53, probably by inhibiting its capacity to activate the transcription from promoters containing a p53-recognition consensus DNA sequence (see  
25 above).

This gene was called the mdmx gene.

The expression of the mdmx gene was investigated by Northern blotting. A polyA+ mRNA blot containing RNA isolated from several mouse tissues was hybridized with a complete mdmx  
30 cDNA-fragment isolated. In all tissues mRNAs of approx. 10 kb and 8 kb were observed. In addition, in testis two strong hybridizing bands of ~ 2000 bp and 1700 bp were seen. These bands are also presents in other tissues but much less abundant. It is unclear as yet what the origin of the longer  
35 mRNAs is. It is thus not excluded that the genomic gene that gives rise to expression of mdmx codes for several, more or less, related proteins that can or cannot bind to p53.

RNA expression of mdmx could also be found by RT-PCR in several mouse tissues and cell lines. Some of the primers from the mouse sequence did also yield a band of expected length with RNA extracted from human cells/cell lines, indicating  
5 already the existence of a human homologue of the mdmx gene. This human PCR fragment was cloned and sequenced. The sequence showed high percentage of identity, but not complete, strongly indicating that part of the human homologue was cloned. In addition, screening of a human cDNA library yielded a cDNA  
10 that also has a high percentage identity with the mouse mdmx cDNA. In total approximately 750 bp of the probable human homologue of mdmx has been cloned and sequenced.

To obtain antisera recognizing the Mdmx protein three synthetic peptides were coupled to BSA and injected both in  
15 rabbits and in mice. We have now obtained one strongly positive polyclonal rabbit antiserum. Mouse sera will be tested and if positive we will try to generate hybridoma's that produce monoclonal antibodies recognizing mdmx protein.

CLAIMS

1. A recombinant or isolated nucleic acid molecule encoding at least a biologically functional part of a mammalian protein capable of binding to a p53 protein and comprising at least a part of the sequence

5  
 1 GTGGCTCTTG CGAACTCTGG GTTTGAGAGG CCGGAAGTGG TGCTGCCGTT  
 51 GCTCGCAGTT TCAAAATGCA GTGCAGGCCT TAGGGTCTCC GGCTGCCACC  
 101 CCTCCCCCAG CTAGGAGGGG GAGCGACTCA TGGAGCGGCC GTAAGTTTGC  
 151 TAACTGTGGA GTCTTCACTG CCAAAATGAC ATCACATTCC ACCTCGGCCC  
 10 201 AGTGTTTCAGC ATCTGACAGT GCTTGCAGAA TTTCTTCGGA ACAAATTAGT  
 251 CAGGTGCGGC CAAAAGTCA GCTTTTGAAG ATTTTGCATG CAGCAGGTGC  
 301 GCAGGGGGAA GTATTACCA TGAAAGAGGT AATGCACTAT CTAGGCCAGT  
 351 ATATAATGGT GAAGCAGCTC TATGATCAAC AGGAGCAACA TATGGTATAC  
 401 TGTGGTGGAG ATCTTTTGGG AGATCTACTT GGATGTCAGA GCTTTTCTGT  
 15 451 GAAAGATCCA AGCCCTCTCT ATGACATGCT AAGAAAGAAT CTTGTTACAT  
 501 CAGCTTCTAA TAACACAGAT GCTGCTCAGA CTCTCGCTCT CGCACAGGAT  
 551 CACACTATGG ATTTTCCAAG TCAAGACCGA CTGAAGCACG GTGCAACAGA  
 601 ATACTCCAAT CCCAGAAAAA GAACTGAAGA AGAGGATACT CACACACTGC  
 651 CTACCTCACG ACATAAATGC AGAGACTCCA GAGCAGATGA AGACTTGATA  
 20 701 GAACATTTAT CTCAAGATGA GACATCTAGG CTTGACCTTG ATTTTGAGGA  
 751 GTGGGACGTT GCTGGCCTGC CTTGGTGGTT TCTAGGGAAT TTGAGAAACA  
 801 ACTGTATTCC TAAAAGTAAT GGCTCAACTG ATTTACAGAC AAATCAGGAT  
 851 ATAGGTACTG CCATTGTTTC AGACACTACG GATGATTTGT GGTTTTTTAA  
 901 TGAGACCGTG TCAGAGCAAT TAGGTGTTGG AATAAAAGTT GAAGCTGCTA  
 25 951 ATTCTGAGCA AACAAGTGAA GTAGGGAAAA CAAGTAACAA GAAGACGGTG  
 1001 GAGGTGGGAA AGGATGATGA TCTTGAGGAC TCCAGGTCCT TGagCGATGA  
 1051 TACTGACGTG GAACTTACCT CTGAGGATGA GTGGCAGTGT ACGGAATGCA  
 1101 AGAAGTTTAA TTCTCCAAGC AAGAGGTACT GTTTTCGTTG CTGGGCCTTG  
 1151 AGAAAGGATT GGTATTCGGA TTGTTCTAAA TTAACATCATT CCCTATCTAC  
 30 1201 ATCTAATATT ACTGCCATAC CTGAAAAGAA GGACAATGAA GGAATTGATG  
 1251 TTCCCGATTG TAGGAGAACC ATTTTCAGCTC CTGTTGTTAG GCCTAAAGAT  
 1301 GGATATTTAA AGGAGGAAAA GCCCAGGTTT GACCCTTGCA ACTCAGTGGG  
 1351 ATTTTGGGAT TTGGCTCATA GTTCTGAAAG CCAGGAGATC ATCTCAAGCG  
 1401 CGAGAGAACA AACAGATATT TTTTCTGAGC AGAAAGCTGA AACAGAAAGT  
 35 1451 ATGGAAGATT TCCAGAATGT CTTGAAGCCG TGTAGCTTAT GTGAAAAAAG  
 1501 GCCTCGGGAT GGGAACATTA TTCATGGGAA GACGAGCCAT CTGACGACAT  
 1551 GTTTCCACTG TGCCAGGAGA CTGAAGAAGT CTGGGGCTTC GTGTCCTGTT  
 1601 TGTAAGAAAG AGATTCAAGT GGTTATTAAA GTTTTATATAG CATAGTTGAG  
 1651 TCAGTCACAG AGAAATACTA GGAGGACCAG GTCATTTATC AAAAAAAAAA  
 40 1701 A

or a functional equivalent thereof.

2. A nucleic acid molecule according to claim 1 which is a cDNA.

3. A nucleic acid molecule according to claim 1 or 2, encoding at least a functional part of the human equivalent of the sequence of claim 1.
4. A recombinant vector comprising a nucleic acid molecule
- 5 according to claims 1-3 together with suitable elements for regulation of replication and/or expression.
5. A recombinant host cell comprising a vector or a nucleic acid molecule according to anyone of the foregoing claims.
6. An isolated or recombinant proteinaceous substance
- 10 comprising at least a biologically functional part of an amino acid sequence resulting from the translation of a nucleic acid molecule according to any one of claims 1-3, the expression of a vector according to claim 4 and/or the culture of a cell according to claim 5.
- 15 7. A method for the identification of proteins having a binding affinity for p53 comprising the steps of labelling a proteinaceous substance comprising at least the binding site of a p53 protein and hybridizing said substance with the protein to be tested.
- 20 8. A method for the identification of nucleic acid molecules encoding proteins having a binding affinity for a p53 protein comprising the steps of expressing said nucleic acid in a suitable expression system, labelling a proteinaceous substance comprising at least the binding site of a p53
- 25 protein and hybridizing said substance with the protein to be tested.



## ABSTRACT

The present invention provides a method to identify new proteins associating to the p53 tumor suppressor protein as well as elucidating the genes encoding said proteins, with some examples of cDNAs isolated this way. It also relates to the results of said method, which are novel proteins having affinity for p53, as well as genes and other nucleic acid molecules encoding these novel proteins.

In particular the invention also provides such a novel protein and its encoding sequences, which protein has homology with the Mdm2 protein and which therefor has been designated as Mdmx.

**Fig 1. Schematic representation of the bacterial p53-expression vector**

**IPTG-inducible  
T7 promoter**

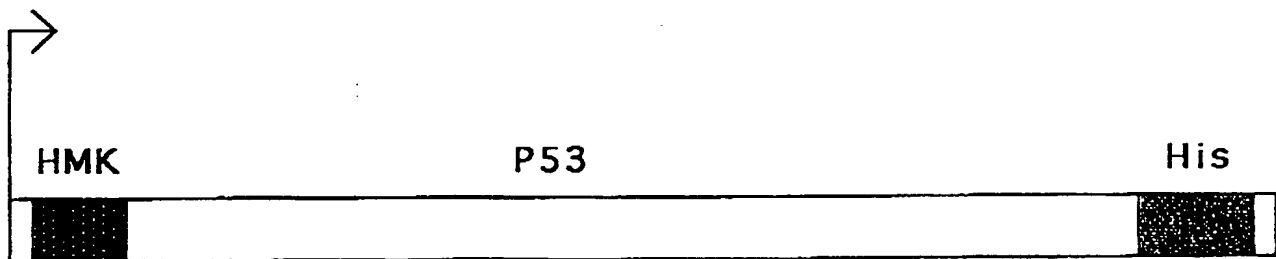


Fig.2 Partial sequence of clone 1 and clone 2

## A. Clone 1

GTATGAGGTGGAAGAAACAGAAGTGGTCATNAAGTCATACCAGAAGAACAGCGATCA  
5 GGATGVNGHAGACAAAAAGAA----- -400 bp----  
GTATGAGGTGGAAGAAACAGAAGTGGTCATNAAGTCATACCAGAAGAACAGCGATCA  
GGATGVNGHAGACAAAAAGAAAGCTTGGGNNCTATTCTATAGTGTACCTAAAGACT  
AGCTTG

## 10 B. Clone 2

CCTTCCGTTGAGGTATGTAGTACCCACTGATACCAGTATTGTAAATGACAGACACTGC  
TTTCTCTGAGGGGAAGTCTGTTTCATTTTTGCACATTCCCGTTTGTA  
----600 bp---CACCACCACACKCACARACACACKCCCAAAAAAAAAACAAAAACA  
15 AACAAACAAAAAAGCTTGGGCCT

A: Adenosine	R: A or G	K: G or T
C: Cytidine	Y: C or T	N: A, C, G or T
20 G: Guanosine	V: A, C or G	
T: Thymidine	H: A, C or T	

**Fig.3 DNA sequence of the mouse mdmx cDNA**

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1  GTGGCTCTTG CGAACTCTGG GTTTGAGAGG CCGGAAGTGG TGCTGCCGTT
51 GCTCGCAGTT TCAAAATGCA GTGCAGGCCT TAGGGTCTCC GGCTGCCACC
101 CCTCCCCCAG CTAGGAGGGG GAGCGACTCA TGGAGCGGCC GTAAGTTTGC
5  151 TAACTGTGGA GTCTTCACTG CCAAAATGAC ATCACATTCC ACCTCGGCCC
201 AGTGTTTCAGC ATCTGACAGT GCTTGCAGAA TTTCTTCGGA ACAAATTAGT
251 CAGGTGCGGC CAAAACTGCA GCTTTTGAAG ATTTTGCATG CAGCAGGTGC
301 GCAGGGGGAA GTATTACCA TGAAAGAGGT AATGCACTAT CTAGGCCAGT
351 ATATAATGGT GAAGCAGCTC TATGATCAAC AGGAGCAACA TATGGTATAC
10 401 TGTGGTGGAG ATCTTTTGGG AGATCTACTT GGATGTCAGA GCTTTTCTGT
451 GAAAGATCCA AGCCCTCTCT ATGACATGCT AAGAAAGAAT CTTGTTACAT
501 CAGCTTCTAA TAACACAGAT GCTGCTCAGA CTCTCGCTCT CGCACAGGAT
551 CACACTATGG ATTTTCCAAG TCAAGACCGA CTGAAGCACG GTGCAACAGA
601 ATACTCCAAT CCCAGAAAAA GAACTGAAGA AGAGGATACT CACACACTGC
15 651 CTACCTCACG ACATAAATGC AGAGACTCCA GAGCAGATGA AGACTTGATA
701 GAACATTTAT CTCAAGATGA GACATCTAGG CTTGACCTTG ATTTTGAGGA
751 GTGGGACGTT GCTGGCCTGC CTTGGTGGTT TCTAGGGAAT TTGAGAAACA
801 ACTGTATTCC TAAAAGTAAT GGCTCAACTG ATTTACAGAC AAATCAGGAT
851 ATAGGTACTG CCATTGTTTC AGACACTACG GATGATTTGT GGTTTTAA
20 901 TGAGACCGTG TCAGAGCAAT TAGGTGTTGG AATAAAAGTT GAAGCTGCTA
951 ATTCTGAGCA AACAAGTGAA GTAGGGAAAA CAAGTAACAA GAAGACGGTG
1001 GAGGTGGGAA AGGATGATGA TCTTGAGGAC TCCAGGTCCT TGagCGATGA
1051 TACTGACGTG GAACTTACCT CTGAGGATGA GTGGCAGTGT ACGGAATGCA
1101 AGAAGTTTAA TTCTCCAAGC AAGAGGTACT GTTTTCGTTG CTGGGCCTTG
25 1151 AGAAAGGATT GGTATTTCGA TTGTTCTAAA TTAATCATT CCCTATCTAC
1201 ATCTAATATT ACTGCCATAC CTGAAAAGAA GGACAATGAA GGAATTGATG
1251 TTCCCGATTG TAGGAGAACC ATTTTCAGCTC CTGTTGTTAG GCCTAAAGAT
1301 GGATATTTAA AGGAGGAAAA GCCCAGGTTT GACCCTTGCA ACTCAGTGGG
1351 ATTTTTGGAT TTGGCTCATA GTTCTGAAAG CCAGGAGATC ATCTCAAGCG
30 1401 CGAGAGAACA AACAGATATT TTTTCTGAGC AGAAAGCTGA AACAGAAAGT
1451 ATGGAAGATT TCCAGAATGT CTTGAAGCCG TGTAAGCTTAT GTGAAAAAAG
1501 GCCTCGGGAT GGGAACATTA TTCATGGGAA GACGAGCCAT CTGACGACAT
1551 GTTTCCACTG TGCCAGGAGA CTGAAGAAGT CTGGGGCTTC GTGTCCTGTT
1601 TGTAAGAAAG AGATTCAAGT GGTATTATAA GTTTTTATAG CATAGTTGAG
35 1651 TCAGTCACAG AGAAATACTA GGAGGACCAG GTCATTTATC AAAAAAAAAA
1701 A

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Fig 4. Amino acid sequence of the putative mouse MDMX protein, and the alignment with the amino acid sequence of mouse MDM2 protein

| = identical amino acid

: = conserved amino acid

The p53-binding domain is depicted in Bold/Italic  
The Zinc-finger motif around position 310-320 and  
the putative Ring finger around position 435-480  
are indicated in Bold

The putative nucleotide binding site (451-453) is  
underlined

	10	20	30	40	50	59
Mdmx	MTSHSTSAQCSASDSACRI-SSEQISQVRPKLQLLKILHAAGAQQEVFTMKEVMHYLGQY					
Mdm2	MCNTNMSVSTEGAASTSQIPASEQETLVRPKPLLLKLLKSVGAQNDTYTMKEIIFYIGQY					
	10	20	30	40	50	60
	60	70	80	90	100	110
Mdmx	IMVKQLYDQQEQHVMVYCGDLLGDLGCSFSVKDPSPLYDMLRKNLV					
Mdm2	IMTKRLYDEKQQHIVYCSNDLLGDVFGVPSFSVKEHRKIYAMIYRNLV					
	70	80	90	100	110	
	120	130	140	150	160	170
Mdmx	LALAQDHTMDFPSQDRLKHGATEYSNPRKRTEEDTHTLPTS					
Mdm2	LSESRRQP--EGGSDLK-DPLQAPPEEKPSDDLISRLSTSSRR-RSISETEENTDELP					
	120	130	140	150	160	170
	180	190	200	210	220	230
Mdmx	--QDETSRLDLDFE-EWDVAGLPWWFLGNLRNNCIPKSNGSTDLQTNQDIGTAIVSDTTD					
Mdm2	GERHRKRRLSLSFDPSLGLCELREMCSSG-TSSSSSSSESTETPSHQDLDDGVSEHSGD					
	180	190	200	210	220	230
	240	250	260	270	280	290
Mdmx	DLWFLNETVSEQLGVGIKVEAANSEQ--TSEVGKTSNKKTVGVGKDDDLSDSRSLSD--D					
Mdm2	CL--DQDSVSDQFSVEFEVESLDSYSLSDGHELSDEDDDEVYRVTVYQTGESDTSFE					
	240	250	260	270	280	290
	300	310	320	330	340	350
Mdmx	TDVELTSEDEWQCTECKKFNSPSKRYCFRCWALRKDWYSDCSKLTHSLSTSNITAIPEK-					
Mdm2	GDPEISLADYWKCTSCNEMNPPLPSHCKRCWTLRENWLPD-DKGKDKVEISEKAKLENSA					
	300	310	320	330	340	
	360	370	380	390	400	410
Mdmx	KDNEGIDVPDCRRRTISAPVVRPKDGYLKEEKPRFDPCNSVGFLDLAHSSSESQEIISSARE					
Mdm2	QAEGLDVPDGKKLTENDAKEPCAEDSEEKAEQTP-LSQESDDYSQPSTSSSIVYSSQE					
	350	360	370	380	390	400

	420	430	440	450	460
Mdmx	QTDIFSEQKAE-TESME-DFQ-NVLKPCSLCEKRPRDGNIIHGKTS	SHLTTCFHCARRLKK			
	:: ::  ::: :  :  :	:::  :  : :::	:::  :  : :::	:::  :  : :::	:::  :  : :::
Mdm2	SVKELKEETQHKDESVESFSLNAIEPCVICQGRPKNGCIVH	GKTGHLMSCFTCAKKLKK			
	410	420	430	440	450
	470	480	490		
Mdmx	SGASCPVCKKEIQLVIKVFIA				
	:: :    :  : ::: :				
Mdm2	RNKPCPVC	RQPIQMIVLSYFN			
	470	480			